

Application No. 09/972,268
Declaration under 37 CFR 1.131

3101-A

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Application No: 09/972,268
Applicants: Peter R. Baum, William C. Fanslow III, Timothy E. Lofton,
Eric A. Sorensen, and Adel Youakim
Filed: October 5, 2001
Title: NECTIN POLYPEPTIDES

TC/Art Unit: 1644
Examiner: Maher M. Haddad

Docket No.: 3101-A

Commissioner for Patents
P.O. Box 1450
Alexandria, VA 22313-1450

DECLARATION UNDER 37 C.F.R. § 1.131

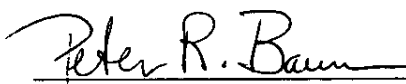
We, Peter R. Baum, William C. Fanslow III, Timothy E. Lofton, Eric A. Sorensen, and Adel Youakim, the undersigned, hereby declare that:

1. This Declaration is made by the inventors of the above-captioned patent application in order to establish a date of invention in the United States prior to April 1, 2000.
2. Prior to April 1, 2000, a DNA clone that encodes human nectin-3 polypeptide (also called "B7L4" polypeptide) had been isolated and its sequence determined in the United States by inventors named in the subject application, as evidenced by the Exhibits A and B enclosed herewith. The works described in Exhibits A and B were completed in this country prior to April 1, 2000.
3. Exhibit A is a copy of a page from one of the laboratory notebooks of Eric A. Sorensen, written in his handwriting, describing a restriction enzyme digest of an isolated lambda phage clone called "HuB7L4 11-1". All dates on the copy have been redacted.

4. Exhibit B (eight pages) is a copy of a computer printout that is incorporated into one of the laboratory notebooks of Eric A. Sorensen, showing the results of the sequencing of the HuB7L4 11-1 clone insert that was performed at the direction of Eric A. Sorensen. The amino acid sequence shown below the corresponding nucleotide sequences is that of human nectin-3 as presented in SEQ ID NO:2 of the above-captioned application (and is identical to amino acids 8 through 549 of SEQ ID NOs 4 and 6). The first page of Exhibit B indicates the location of a predicted signal sequence cleavage site, and the fourth page of Exhibit B indicates the location of the start of the transmembrane domain. All dates on the copy have been redacted.

5. Therefore, on a date prior to April 1, 2000, the inventors of the above-captioned application had determined the amino acid sequence of a human nectin-3 polypeptide including the extracellular domain of a mature form of human nectin-3.

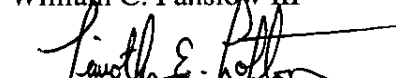
6. As a person signing below: I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code, and that such willful false statements may jeopardize the validity of the application or any patent issued thereon.


Peter R. Baum

Date: July 7, 2003


William C. Fanslow III


Date: June 23, 2003


Timothy E. Lofton

Date: 23 JUNE 2003


Eric A. Sorensen

Date: June 24, 2003

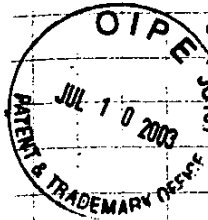

Adel Yezakim

Date: June 24, 2003

rom Page No. 77

Ø DNA for HUB7C4 picks 11-1 and 13 (from KB library)
sat in PEG for the 3 weeks I was on vacation.

Spun out Washed 1x 70% EtOH. Spun out
out heat. Resuspended o/n in 60 µl H₂O.



Digest Ø DNAs w/ EcoRI (NEB rxn buffer) and w/ NotI (NEB buffer, Bm)

1.) Ø DNA 11-1 w/ EcoRI

2.) " " w/ NotI

3.) Ø DNA 13 w/ EcoRI

4.) " " w/ NotI

4 µl Ø DNA

1.5 µl 10x Buffer

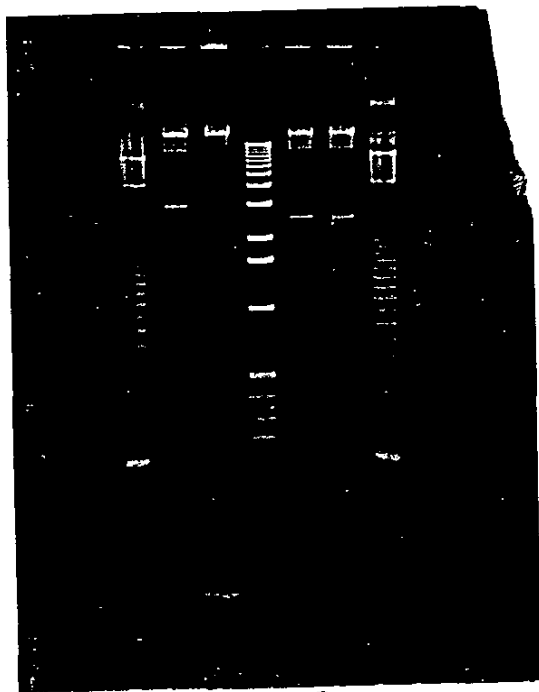
.5 µl enzyme

9 µl H₂O

37°C 60-90'

11-1 (c) 95.5 µg/ml

13 (c) 57.7 µg/ml



7055 p.80 GAS

RESULTS:

According to this gel, the clone #13 is way smaller compared to what I estimated by sequence & Pch. I guess I'll see what the DNA size like and I'm going to subclone the EcoRI fragment into pBS.

To Page No. 8

Witnessed & Understood by me,

Barry M. [Signature]

Date

Invented by

Recorded by

Date

Hub7L4 #11 from KB library clone #11-1. Phage DNA: **NOT CONFIRMED**
 sr6527 R. Sorensen
 /bertlesj/sorensen/sr6527/hub7l4-11.seq
 8139,8140,DPC#9117-20,12233-34,12759-60,12801
 Hub7L4-11

WI
O I P E
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NspI
 AflIII
 BspLUIII
 MslI
 181 **ATTGTGGAGCCACATGTCACAGCAGTATGGGGAAAGAATGTTTCATTAAAGTGTTTAATT** 240

77,85 p 8

```

TAACACCTCGGTGTACAGTGTGTCATACCCCTTTCTTACAAAGTAATTTACAAATTAA
      ← 34054
a   I V E P H V T A V W G K N V S L K C L I -

      33686 →
GAAGTAAATGAAACCATAACACAGATTTTCATGGGAGAAGATACATGGCAAAAGTTCACAG
241 -----+-----+-----+-----+-----+-----+-----+ 300
a   CTTCAATTTACTTTGGTATTGTGTCTAAAGTACCCTCTTCTATGTACCGTTTTCAAGTGTC
    E V N E T I T Q I S W E K I H G K S S Q -

      XcmI      AhoI      EarI
      |         |         |
ACTGTTGCAGTTCACCATCCCCAATATGGATTCTCTGTTCAAGGAGAATATCAGGGAAGA
301 -----+-----+-----+-----+-----+-----+-----+ 360
a   TGACAACGTCAAGTGGTAGGGTTATACCTAAGAGACAAGTTCCTCTTATAGTCCCTTCT
    ← 33685
    T V A V H H P Q Y G F S V Q G E Y Q G R -

      DraI
      |
GTCTTGTTTAAAAATTACTCACTTAATGATGCAACAATTACTCTGCATAACATAGGATTC
361 -----+-----+-----+-----+-----+-----+-----+ 420
a   CAGAACAAATTTTTTAATGAGTGAATTACTACGTTGTTAATGAGACGTATTGTATCCCTAAG
    V L F K N Y S L N D A T I T L H N I G F -

      BmrI
      |
TCTGATTCTGGAAAATACATCTGCAAAGCTGTTACATTCCCGCTTGGAAATGCCAGTCC
421 -----+-----+-----+-----+-----+-----+-----+ 480
a   AGACTAAGACCTTTTATGTAGACGTTTCGACAATGTAAGGGCGAACCTTTACGGGTCAGG
    ← 33687
    S D S G K Y I C K A V T F P L G N A Q S -

TCTACAACTGTAAGTGTGTTAGTTGAACCCACTGTGAGCCTGATAAAGGGCCAGATTCT
481 -----+-----+-----+-----+-----+-----+-----+ 540
a   AGATGTTGACATTGACACAATCAACTGGGTGACACTCGGACTATTTTCCCGGTCTAAGA
    S T T V T V L V E P T V S L I K G P D S -

      AlwNI
      |
TTAATTGATGGAGGAAATGAAACAGTAGCAGCCATTTGCATCGCAGCCACTGGAAAACCC
541 -----+-----+-----+-----+-----+-----+-----+ 600
a   AATTAACCTACCTCCTTTACTTTGTCATCGTCGGTAAACGTAGCGTCGGTGACCTTTTGGG
    L I D G G N E T V A A I C I A A T G K P -

      BmrI
      |
32121 →
GTTGCACATATTGACTGGGAAGGTGATCTTGGTGAAATGGAATCCACTACAACCTCTTTT
601 -----+-----+-----+-----+-----+-----+-----+ 660
a   CAACGTGTATAACTGACCCTTCCACTAGAACCACTTTACCTTAGGTGATGTTGAAGAAAA
    ← 33688
    V A H I D W E G D L G E M E S T T T S F -

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TatI
|

661 -----+-----+-----+-----+-----+-----+-----+ 720
 CCAAATGAAACGGCAACGATTATCAGCCAGTACAAGCTATTTCCAACCAGATTGCTAGA
 a GGTTTACTTTGCCGTTGCTAATAGTCGGTCATGTTTCGATAAAGGTTGGTCTAAACGATCT
 P N E T A T I I S Q Y K L F P T R F A R -

MmeI BsbI StyI
| | |

721 -----+-----+-----+-----+-----+-----+ 780
 GGAAGGCGAATTACTTGTGTTGTAAAACATCCAGCCTTGGAAAAGGACATCCGATACTCT
 CCTTCGCGCTTAATGAACACAACATTTTGTAGGTCGGAACCTTTTCCTGTAGGCTATGAGA
 ← 32122
 a G R R I T C V V K H P A L E K D I R Y S -

Eco57I
|

781 -----+-----+-----+-----+-----+-----+ 840
 TTCATATTAGACATACAGTATGCTCCTGAAGTTTCGGTAACAGGATATGATGGAAATTGG
 a AAGTATAATCTGTATGTCATACGAGGACTTCAAAGCCATTGTCCTATACTACCTTTAACC
 F I L D I Q Y A P E V S V T G Y D G N W -

BsaBI MmeI
| |

841 -----+-----+-----+-----+-----+-----+ 900
 TTTGTAGGAAGAAAAGGTGTTAATCTCAAATGTAATGCTGATGCAAATCCACCACCCTTC
 a AAACATCCTTCTTTTCCACAATTAGAGTTTACATTACGACTACGTTTAGGTGGTGGGAAG
 F V G R K G V N L K C N A D A N P P P F -

Eco57I
|

BspMI HaeI
| |

901 -----+-----+-----+-----+-----+-----+ 960
 AAATCTGTGTGGAGCAGGTTGGATGGACAATGGCCTGATGGTTTATTGGCTTCAGACAAT
 a TTTAGACACACCTCGTCCAACCTACCTGTTACCGGACTACCAAATAACCGAAGTCTGTTA
 K S V W S R L D G Q W P D G L L A S D N -

EarI
|

961 -----+-----+-----+-----+-----+-----+ 1020
 ACTCTTCATTTTGTCCATCCATTGACTTTCAATTATTCTGGTGTATATCTGTAAAGTG
 a TGAGAAGTAAAACAGGTAGGTAAGTAAAGTAAATAAGACCACAAATATAGACATTTTAC
 T L H F V H P L T F N Y S G V Y I C K V -

StyI DrdI BstYI Eco57I
| | |

1021 -----+-----+-----+-----+-----+-----+ 1080
 ACCAATTCCTTGGTCAAAGAAGTGACCAAAAAGTCATCTACATTTTCAGATCCTCCTACT
 a TGGTTAAGGGAACCGAGTTTCTTCACTGGTTTTTCAGTAGATGTAAAGTCTAGGAGGATGA
 T N S L G Q R S D Q K V I Y I S D P P T -

BstYI
|

1081 ACTACCACCCTTCAGCCTACAATTCAAGTGGCATCCCTCAACTGCTGACATCGAGGATCTA 1140
-----+-----+-----+-----+-----+
TGATGGTGGGAAGTCGGATGTTAAGTCACCGTAGGGAGTTGACGACTGTAGCTCCTAGAT
a T T T L Q P T I Q W H P S T A D I E D L -

HincII
|

1141 GCAACAGAACCTAAAAAATTGCCCTTCCCATTGTCAACTTTGGCAACAATTAAGGATGAC 1200
-----+-----+-----+-----+-----+
CGTTGTCTTGGATTTTTTAACGGGAAGGGTAACAGTTGAAACCGTTGTTAATTCCTACTG
a A T E P K K L P F P L S T L A T I K D D -

ScaI
|

TaqII BanII TatI
| | | |
MunI BsrDI(Bgl2) Bsp1286I EarI | | |
| | | | | | |

1201 ACAATTGCCACGATCATTGCTAGTGTAGTGGGTGGGGCTCTCTTCATAGTACTTGTAAGT 1260
-----+-----+-----+-----+-----+
TGTTAACGGTGCTAGTAACGATCACATCACCCACCCGAGAGAAGTATCATGAACATTCA
TGTTAACGGTGC-TCTAGA ←32124
Start Transmembrane ^ <--34357
a T I A T I I A S V V G G A L F I V L V S -

Bsp24I
|

SspI SfcI BbsI Bsp24I
| | | |

1261 GTTTTGGCTGGAATATTCTGCTATAGGAGAAGACGGACGTTTCGTGGAGACTACTTTGCC 1320
-----+-----+-----+-----+-----+
CAAAACCGACCTTATAAGACGATATCCTCTTCTGCCTGCAAAGCACCTCTGATGAAACGG
a V L A G I F C Y R R R R T F R G D Y F A -

AAGAACTACATTCCACCATCAGATATGAAAAAGAATCACAAATAGATGTTCTTCAACAA
1321 -----+-----+-----+-----+-----+ 1380
TTCTTGATGTAAGGTGGTAGTCTATACGTTTTTCTTAGTGTATCTACAAGAAGTTGTT
← 32125
a K N Y I P P S D M Q K E S Q I D V L Q Q -

GATGAGCTTGATTCTTACCCAGACAGTGTAAAAAAGAAAACAAAATCCAGTGAACAAT
1381 -----+-----+-----+-----+-----+ 1440
CTACTCGAACTAAGAATGGGTCTGTCACATTTTTTCTTTTGTGTTTGTAGGTCCTTGTTA
a D E L D S Y P D S V K K E N K N P V N N -

BsaAI EarI
| |
SnaBI SapI
| |

1441 CTAATACGTAAAGACTATTTAGAAGAGCCTGAAAAAACTCAGTGAACAATGTAGAAAAT 1500
-----+-----+-----+-----+-----+
GATTATGCATTTCTGATAAATCTTCTCGGACTTTTTTGAGTCACCTTGTTACATCTTTTA
a L I R K D Y L E E P E K T Q W N N V E N -

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                                BglII
                                BstYI
                                |
CTCAATAGGTTTGAAAGACCAATGGATTATTATGAAGATCTAAAAATGGGAATGAAGTTT
1501 -----+-----+-----+-----+-----+ 1560
a   GAGTTATCCAAACTTTCTGGTTACCTAATAATACTTCTAGATTTTTTACCCTTACTTCAAA
    L N R F E R P M D Y Y E D L K M G M K F -

                                MslI
                                NspI|
                                AflIII
                                BspLU11I| | DrdII
                                MslI| | |
GTCAGTGATGAACATTATGATGAAAACGAAGATGACTTAGTTTCACATGTAGATGGTTCC
1561 -----+-----+-----+-----+-----+ 1620
a   CAGTCACTACTTGTAACTACTTTTTGCTTCTACTGAATCAAAGTGACATCTACCAAGG
    V S D E H Y D E N E D D L V S H V D G S -

                                BsrGI
                                TatI
                                (NotI)
GTAATTTCCAGGAGGGAGTGGTATGTTTAGCAACCACTGAATGTGACTTAACTATGTACA
1621 -----+-----+-----+-----+-----+ 1680
a   CATTAAGGTCCTCCCTCACCATACAAATCGTTGGTGACTTACACTGAATTGATACATGT
    <--34358 -CGCCGGCG
    V I S R R E W Y V * <--36018

                                SpeI BclI
                                | |
ATGTTTCATTCACACTAGTTGATCATTTCAGATTGTTTCATACTTTTTCTTGAGGAAGAAT
1681 -----+-----+-----+-----+-----+ 1740
a   TACAAGTAAGTGTGATCAACTAGTAAAAGTCTAACAAGTATGAAAAGAAGTCTCTCTTA

HindIII Bce83I HindIII
| | |
AAGCTTTTCAAGTTGATTTTCAAGCTTACTTTTTATATTCTAATCTGACAAATGAAAAAT
1741 -----+-----+-----+-----+-----+ 1800
a   TTCGAAAAAGTTCAACTAAAAGTTCGAATGAAAAATATAAGATTAGACTGTTTACTTTTA

                                TatI
                                Bce83I|
                                | |
GTAAAAATCTGAGTTCAGTGTATCTAAGCTGCTTTACAATTTTTTTTTCAATGCTGTACTAC
1801 -----+-----+-----+-----+-----+ 1860
a   CATTTTAGACTCAAGTCACATAGATTCGACGAAATGTTAAAAAAAAGTTACGACATGATG

                                ApoI
                                DraI|
                                ScaI
SmlI SwaI| | TatI| |
| | |
TGTCTCAAGATTTAAATTTTAATGCAGAGTACTTTATTGGTGTGAGGCACACAGGTAAGA
1861 -----+-----+-----+-----+-----+ 1920

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ACAGAGTTCTAAATTTAAAATTACGTCTCATGAAATAACCACACTCCGTGTGTCCATTCT

HincII ApoI DraI

AGAAATGTCAACATTAAATGTATGACTTACTTGGTACAAAAATTTTAAAGGGAAGT

1921 -----+-----+-----+-----+-----+-----+-----+ 1980

TCTTTACAGTTGTAATTTACATACTGAATGAACCATGTTTTTAAAAAATTTTCCCTTGA

Bce83I Tth111II SmlI

ACCTTGACATTGTGTATTAAATGTTTACCTAAGACTATAATCTCAAGTATGATGTTTGT

1981 -----+-----+-----+-----+-----+-----+-----+ 2040

TGGAAGTGTAAACATAATTTACAAATGGATTCTGATATTAGAGTTCATACTACAAACAA

BtsI HaeIV Hin4I ApoI

TAACATATACCTCTCAAAATTTATCACCCTCAATGACACTGCATCAAAATTGACTATAA

2041 -----+-----+-----+-----+-----+-----+-----+ 2100

ATTGTATATGGAGAGTTTTTAAATAGTGGTGAGTTACTGTGACGTAGTTTTTAACGTATATT

SspI SspI

AACTAATTCAAGAAATATTTATATATATTTTTTAATATACAAAAATATTTAGCCTGATG

2101 -----+-----+-----+-----+-----+-----+-----+ 2160

TTGATTAAGTTCTTTATAAATATATATAAAAAATTATATGTTTTTTATAAATCGGACTAC

Tth111II

GAATGGCTTTCCTTTTCAAACATTATTTTCTAAGTTTCTATACAAATGAAATCTTTACCT

2161 -----+-----+-----+-----+-----+-----+-----+ 2220

CTTACCGAAAGGAAAAGTTTGTAAATAAAGATTCAAAGATATGTTTACTTTAGAAATGGA

MslI VspI SfcI

CTGCATATTAATGAGCCTTGCCATAATTACTGTAGAGTGGCTTTTCAAAGATATTTTGT

2221 -----+-----+-----+-----+-----+-----+-----+ 2280

GACGTATAATTACTCGGAACGGTATTAATGACATCTCACCGAAAAGTTTCTATAAAACAA

EarI SapI

GCACTAAACTGTGGTAGTAAACTCAGTGAACATGATGTGTGGAAGAGCATAATTAGCTG

2281 -----+-----+-----+-----+-----+-----+-----+ 2340

CGTGATTTTGACACCATCATTTGAGTCACTTGTACTACACACCTTCTCGTATTAATCGAC

SspI BspMI

GTCAATATTTTTGTCCAAAATACCTGCAAGAGTAATAAAATACATACCTTTCAAACATGA

2341 -----+-----+-----+-----+-----+-----+-----+ 2400

CAGTTATAAAAAACAGGTTTTATGGACGTTCTCATTATTTTATGTATGGAAAGTTTGTACT

```

Tth1111I
|
TAATTATTAGTTTTTTTTTTCCTTTCTGGAACATGGATTTTGGTACATTAGCAGTAGCCT
2401 -----+-----+-----+-----+-----+-----+-----+ 2460
ATTAATAATCAAAAAAAAAAAGGAAAGACCTTGACCTAAAACCATGTAATCGTCATCGGA

TATTTTAATGCTTTTATGTCCTAAACATACTAATAGAAATGAAAAGACGCAGAGAGAGCAT
2461 -----+-----+-----+-----+-----+-----+-----+ 2520
ATAAAATTACGAAATACAGGATTTGTATGATTATCTTTACTTTTCTGCGTCTCTCTCGTA

                               SpeI
                               ScaI|
                               TatI |||                               Eco57I                               SfcI                               ApoI
                               | |||                               |                               |                               |
TTCGGAATACTGAAGTACTAGTTTTAGAAATGAGACTTTCAGCCAACAATCTATAGAAAG
2521 -----+-----+-----+-----+-----+-----+-----+ 2580
AAGCCTTATGACTTCATGATCAAAATCTTTACTCTGAAAGTCGGTTGTTAGATATCTTTC

                                               BsrGI
                                               TatI
                                               |
AATTTTATGGACCATCTTGTTTTAGTTATTTAATGTTGATGTTGTTCAAATGGGTAAATG
2581 -----+-----+-----+-----+-----+-----+-----+ 2640
TTAAATACCTGGTAGAACAAAATCAATAAATTACAAC TACAACAAGTTTACCCATTTAC

ApoI
|
TACAGAAAGAAAATTTTAGAGTAAACTTGGAACCTTGGATATAACTAGAAAAAACTAGAT
2641 -----+-----+-----+-----+-----+-----+-----+ 2700
ATGTCCTTCTTTTAAATCTCATTGTAACCTTGAAACCTATATTGATCTTTTTTGATCTA

                               BsmI
                               |
TATAGAATTAGTCGGTAACACTTGCTAATGGACATTGGCATTTCATCTCCTTTTTCTCCT
2701 -----+-----+-----+-----+-----+-----+-----+ 2760
ATATCTTAATCAGCCATTGTGAACGATTACCTGTAACCGTAAGTAGAGGAAAAAGGAGGA

AAGTGTATGTATGTGTTTTAAGATTTCTGTTTTTACGATTAAAACTGGAACATGAGGTT
2761 -----+-----+-----+-----+-----+-----+-----+ 2820
TTCACATACATACACAAAATTCTAAAGACAAAAATGCTAATTTTGACCTTTGTACTCCAA

TTTTGTTTTTGTTTTTTTACATAATTACATATATTCCTTCTGAATCATTTATCTTTTGAG
2821 -----+-----+-----+-----+-----+-----+-----+ 2880
AAAACAAAAACAAAAAATGTATTAATGTATATAAGGAAGACTTAGTAAATAGAAAACTC

Tth1111I                               SfcI
|                               |
AAAGAAATGTTACCTAACTTCAAATGTGCTTTTTGTTTGTGAGGTAATTAAATTGCTTC
2881 -----+-----+-----+-----+-----+-----+-----+ 2940
TTTCTTTACAATGGATTTGAAGTTTACACGAAAAACAAACACTCCATTAATTTAACGAAG

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TACAGTGGAGGCTTACAAAATTATTGTGACAACATTTTGAAGCTGAAAGGATAGTTTTT
2941 -----+-----+-----+-----+-----+-----+ 3000
ATGTCACCTCCGAATGTTTAAATAACACTGTTGATAAACTTCGACTTTCCTATCAAAAA

CTATTGCTAAGTCATTTGAAAAAGTGACCATTTTGCCAGTGAAATGAAGTGGAAGTTAGT
3001 -----+-----+-----+-----+-----+-----+ 3060
GATAACGATTTCAGTAACTTTTCACTGGTAAAACGGTCACTTTACTTCACCTTCAATCA

AGGAGAATCATAAATTAAATATATTATTTTGTTAATAAAAAAGGCAAAGTAGTAGGTACTT
3061 -----+-----+-----+-----+-----+-----+ 3120
TCCTCTTAGTATTTAATTTATATAATAAAACAATTATTTTCCGTTTCATCATCCATGAA

                                     ApoI
                                     EcoRI
                                     BsiEI
                                     EaeI
                                     EagI
                                     GdiII
                                     NotI
                                     MspAII
DraI                               SspI
|                                 |
TTTAAACCCTCCCAACCAGCCCTTTCTCAATATTCATCAAATCTAAACAGCGGCCGCGA
3121 -----+-----+-----+-----+-----+-----+ 3180
AAATTTGGGAGGGTTGGTCGGGAAAGAGTTATAAGTAGTTTAGATTTTGTGCGCCGGCGCT

ATTCAGC
3181 ----- 3187
TAAGTCG

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Enzymes that do cut:

AflIII	AloI	AlwNI	ApoI	BanI	BanII	BbsI	Bce83I
BclI	BglII	BmrI	BplI	BpmI	Bpu10I	BsaAI	BsaBI
BsaHI	BsaXI	BsbI	BseRI	BsiEI	BsmI	Bsp24I	Bsp1286I
BspGI	BspLU11I	BspMI	BsrDI	BsrGI	BstYI	BtsI	DraI
DrdI	DrdII	EaeI	EagI	EarI	Eco57I	EcoRI	GdiII
HaeI	HaeIV	Hin4I	HincII	HindIII	MmeI	MslI	MspAII
MunI	NotI	NspI	PstI	SapI	ScaI	SfcI	SmlI
SnaBI	SpeI	SspI	StyI	SwaI	TaqII	TatI	Tth111III
VspI	XcmI						

Enzymes that do not cut:

AarI	AatII	AccI	AceIII	AclI	AflII	AhdI	ApaI
ApaLI	AscI	AvaI	AvrII	BaeI	BamHI	BbvCI	BcgI
BciVI	BglI	BmgI	Bpu1102I	BsaI	BsaWI	BseSI	BsgI
BsiHKAII	BsmBI	BspEI	BsrBI	BsrFI	BssHII	BssSI	BstAPI
BstDSI	BstEII	BstXI	BstZ17I	Bsu36I	ClaI	DraIII	EciI
Eco47III	EcoNI	EcoO109I	EcoRV	FseI	FspI	HaeII	HgiEII
HpaI	KpnI	MluI	MscI	NarI	NcoI	NdeI	NgoAIV
NheI	NruI	NsiI	NspV	PacI	Pfl1108I	PflMI	PinAI
PmeI	PmlI	PpiI	PshAI	Psp5II	PvuI	PvuII	RcaI
RleAI	RsrII	SacI	SacII	SalI	SanDI	SbfI	SexAI
SfiI	Sgfi	SgrAI	SmaI	SphI	SrfI	Sse8647I	StuI
SunI	Tth111I	XbaI	XhoI	XmnI			